OM of: US-08-911-423-2 to: N_Geneseq_34:*   out_format : pfs
Date: Aug 5, 1999   2:43 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US08911423/runat_05081999_084745_1154/app_query.fasta.1
-DB=N_Geneseq_34 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=escore
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=stat -USER=US08911423
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Search information block:
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Query length: 228
Database: N_Geneseq_34:*
Database sequences: 240622
Database length: 94065609
Search time (sec): 110.750000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
N_Geneseq_34:V32773	+	1195.00	2631.41	4.4e-139	1020	Mouse glucocorticoid induced T
N_Geneseq_34:V19152	+	1195.00	2630.87	4.7e-139	1073	Nucleotide sequence of the mou
N_Geneseq_34:V32772	+	1161.50	2556.76	6.3e-135	1031	Mouse GITR-B cDNA. New isolate
N_Geneseq_34:V32775	+	1155.00	2541.73	4.4e-134	1087	Mouse GITR-C cDNA. New isolate
N_Geneseq_34:V19153	+	660.50	1442.32	7.5e-73	1006	Nucleotide sequence of the hum
N_Geneseq_34:V19154	+	509.50	1109.90	2.5e-54	723	Truncated human 312C2 protein
N_Geneseq_34:086126	+	176.00	366.29	6.5e-13	838	H4-1BB receptor protein cDNA. N
N_Geneseq_34:075424	+	176.00	360.66	1.3e-12	1415	Human 4-1BB polypeptide coding
N_Geneseq_34:T91026	+	176.00	360.66	1.3e-12	1415	Human 4-1BB receptor cDNA clon
N_Geneseq_34:T88969	+	174.00	360.53	1.4e-12	946	DNA encoding a human h4-1BBSV I
N_Geneseq_34:T39546	+	157.00	324.01	1.5e-10	838	Human receptor H4-1BB cDNA. Mon
N_Geneseq_34:092086	+	158.00	320.43	2.3e-10	1439	Human 4-1BB induced by lymp
N_Geneseq_34:075428	+	153.50	317.16	3.5e-10	768	Murine 4-1BB polypeptide encod
N_Geneseq_34:T91027	+	153.50	317.16	3.5e-10	768	Mouse 4-1BB receptor cDNA clone
N_Geneseq_34:T39541	+	153.50	305.16	1.6e-09	2347	Mouse receptor 4-1BB cDNA. Mon
N_Geneseq_34:086127	+	153.50	305.15	1.7e-09	2350	4-1BB receptor protein cDNA. N
N_Geneseq_34:T00826	+	113.50	230.50	2.4e-05	618	Mouse type-II membrane polypept
N_Geneseq_34:T32640	+	113.50	230.50	2.4e-05	618	Mouse OX40 extracellular domain
N_Geneseq_34:T00829	+	117.00	230.16	2.5e-05	1317	Plasmid pDC406/OX40/Fc* encodi
N_Geneseq_34:V32636	+	117.00	230.16	2.5e-05	1317	OX40/Fc cDNA. Purified polypep
N_Geneseq_34:V41379	+	115.50	223.01	6.2e-05	1878	Murine NF-kB receptor activato
N_Geneseq_34:V41373	+	115.50	223.01	6.2e-05	1878	Murine NF-kB receptor activato
N_Geneseq_34:V41375	+	109.00	211.77	0.0003	1391	RANK partial polypeptide encod
N_Geneseq_34:V41369	+	109.00	211.77	0.0003	1391	RANK partial polypeptide encod
N_Geneseq_34:088758	+	105.00	205.82	0.0006	1057	ACT-4 cell surface receptor cD
N_Geneseq_34:T04048	+	105.00	205.82	0.0006	1057	ACT-4-h-1 receptor cDNA sequen
N_Geneseq_34:V41370	+	109.00	203.04	0.0008	3136	NF-kB receptor activator RANK
N_Geneseq_34:Q93257	+	101.00	199.47	0.0013	834	Human OX-40 cDNA. Nucleic acid
N_Geneseq_34:T33166	+	102.00	198.88	0.0014	1083	Mutated OCIF, OCIF-DCR1, coding
N_Geneseq_34:T33174	+	100.50	198.55	0.0014	819	Mutated OCIF, OCIF-CDD2, coding
N_Geneseq_34:V62467	+	106.00	197.66	0.0016	2781	Human dendritic cell receptor
N_Geneseq_34:T33171	+	100.50	196.78	0.0018	966	Mutated OCIF, OCIF-CSph, coding
N_Geneseq_34:T33173	+	100.50	196.58	0.0018	984	Mutated OCIF, OCIF-DDD2, coding
N_Geneseq_34:T35475	+	100.50	195.82	0.0020	1056	Mutated OCIF, OCIF-CC, coding
N_Geneseq_34:T33178	+	100.50	194.69	0.0023	1173	Human tumour necrosis factor I
N_Geneseq_34:V24487	+	100.50	194.61	0.0024	1182	Mutated OCIF-CBst, codin
N_Geneseq_34:T33172	+	100.50	194.55	0.0024	1188	Modified TR1 receptor coding s
N_Geneseq_34:T33163	+	100.50	194.45	0.0024	1200	Mutated OCIF, OCIF-CL, coding
N_Geneseq_34:T33164	+	100.50	194.39	0.0024	1206	Mutated OCIF, OCIF-C21S, codin
N_Geneseq_34:T33165	+	100.50	194.39	0.0024	1206	Mutated OCIF, OCIF-C22S, codin
N_Geneseq_34:T36685	+	100.50	194.39	0.0024	1206	Osteoclastogenesis inhibito
N_Geneseq_34:V20768	+	100.50	194.39	0.0024	1206	Human OCIF genome cDNA. Inh
N_Geneseq_34:T96063	+	100.50	193.14	0.0029	1355	Human osteoprotegerin cDNA.

seq_name: N_Geneseq_34:V32773

seq_documentation_block:
ID V32773 standard; cDNA; 1020 BP.
AC V32773;
DT 29-SEP-1998 (first entry)
DE Mouse glucocorticoid induced TNFR-family related protein cDNA.
KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
KW GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B.
KW GITR-C; ds.
OS Mus sp.
FH Key   Location/Qualifiers
FT CDS   46..732
FT   /*tag= a
FT   /product= "Mouse GITR"
FT sig_peptide   46..102
FT   /*tag= b
PN WO9824895-A1.
PD 11-JUN-1998.
PF 08-NOV-1997; E06252.
PR 02-DEC-1996; GB-025074.
PA (PHAA) PHARMACIA & UPJOHN SPA.
PI Riccardi C;
DR WPI; 98-333315/29.
DR P-PSDB; W49016.
PT New isolated glucocorticoid induced TNFR related polypeptide - used
PT to stimulate lymphocyte activity and cell death rescue, useful to,
PT e.g. develop products to suppress lymphocyte activity and induce
PT apoptosis
PS Claim 1; Pages 34-36; 53pp; English.
CC The present claimed sequence represents a mouse glucocorticoid
CC induced TNFR-family related protein (GITR) cDNA isolated from a
CC mouse T-cell cDNA library. The invention also claims variants of
CC (V32774) and GITR-C (V32775) cDNAs which are splicing variants of
CC GITR cDNA. The GITRs are claimed to be useful for stimulating lymphocyte
CC activity and cell death rescue. GITR antagonists are claimed to be
CC useful for suppressing the lymphocyte activity and for inducing
CC apoptotic deletion. GITR cDNAs and the proteins they encode are
CC also claimed to be useful for suppressing growth of tumour cells
CC over-expressing GITR or for the treatment of refractory hodgkin's
CC disease.
SQ Sequence   1020 BP;   231 A;   269 C;   292 G;   228 T;

alignment_scores:
         Quality: 1195.00   Length: 228
           Ratio: 5.241   Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-08-911-423-2 x V32773   ..

Align seg 1/1 to: V32773 from: 1 to: 1020

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 46 ATGGGGGCATGGGCCATGCTGTATGGAGTCTCGATGCTCTGTGTGCTGGA  95

 17 pLeuGlyGlnProSerValValGluProGlyCysGlyProGlyLysV  34
    ||||||||||||||||||||||||||||||||||||||||||||||||
 96 CCTAGGTGCCAGTGAGTGTAGTTGAGGAGCCTGGCCTGGCCCTGGCAAGG  145

 34 aIGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaPro  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
146 TTCAGAACGGAAGTGGCAACAACACTCGCTGCTGCAGCCTGTATGCTCCA  195

 51 GlyLysGluAspCysProLysGluArgCysIleCysValThrProGluTy  67
    ||||||||||||||||||||||||||||||||||||||||||||||||||
196 GGCAAGGAGGACTGTCCAAAAGAAAGGTGCATATGTGTCACACCTGAGTA  245
```

CC   of 312C2 stimulates proliferation of T cell clones, antigen-specific
CC   proliferation and cytokine production by T-cells, and potentiates T
CC   cell expansion or apoptosis. The products can be used in the
CC   treatment of conditions associated with abnormal physiology or
CC   development, including abnormal proliferation, e.g. cancerous
CC   conditions or degenerative conditions. They can be used in the
CC   regulation or development of haematopoietic cells, e.g. lymphoid cells
CC   which affect immunological responses, e.g. autoimmune disorders.
SQ   Sequence 1073 BP;   243 A;   283 C;   310 G;   237 T;

alignment_scores:
　　　　　Quality: 1195.00　　　　　　　Length:　　228
　　　　　Ratio:　　 5.241　　　　　　　　Gaps:　　　　0
Percent Similarity: 100.000　　Percent Identity: 100.000

alignment_block:
US-08-911-423-2 x V19152
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Align seg 1/1 to: V19152 from: 1 to: 1073

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 68 ATGGGGGCCATGGCCATGCTGTATGGAGTCTCAGATGCTCTGTGTGCTGGA 117

 17 pLeuGlyGlnProSerValValGluValProGlyCysGlyProGlyLysV  34
    |||||||||||||||||||||||||||||||||||||||||||||||||||
118 CCTAGGTCAGGCCAGTGTAGTTGAGGAGCCTGGCTGTGGCCCTGGCAAGG 167

 34 aIGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaPro  50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
168 TTCAGAACGGAAGTGGCAACAACACTCGCTCGTGCTGCTCTGTATGCTCCA 217

 51 GlyLysGluAspCysProLysGluCysIleCysValThrProGluTy  67
    |||||||||||||||||||||||||||||||||||||||||||||||||||
218 GGCAAGGAGGACTGTCCAAAAGAAAGGTGCATATGTGTCACACCTGAGTA 267

 67 rHisCysGlyAspProGlnCysLysLysHisTyrProCysGlnP  84
    |||||||||||||||||||||||||||||||||||||||||||||||||||
268 CCACTGTGCAGGACCCTCAGTGCAAGATCTGCAAGCACTACCCCTGCCAAC 317

 84 roGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
    |||||||||||||||||||||||||||||||||||||||||||||||||||
318 CAGGCCCAGAGGGTGGAGTCTCAAGGGGATATTGTGTTTGGCTTCCGGTGT 367

101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysAr 117
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368 GTTGCCTGCGCCATGGGCACCTTCTCCGCAGGTCGTGACGGTCACTGCAG 417

117 gLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyA 134
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418 ACTTTGGACCAACTGTTCTCAGTTTGGATTTCTCACCATGTTCCCTGGGA 467

134 snLysThrHisAsnAlaValCysIleProLeuProThrGluGln 150
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468 ACAAGACCCACAATGCTGTGTGCATCCCGGAGCCACTGCCCACTGAGCAA 517

151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePh 167
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518 TACGGCCATTTGACTGTCATCTTCCTGGTCATGGCTGCATGCATTTTCTT 567

167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
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568 CCTAACCACAGTCCAGCTCGGCCTGCACATATGGCAGCTGAGGAGGCAAC 617

184 isMetCysProArgGluThrGlnProPheAlaGlnValGlnLeuSerAla 200
    |||||||||||||||||||||||||||||||||||||||||||||||||||
618 ACATGTGTCCCGAGAGACCCAGCCATTCGCGAGGTGCAGTTGTCAGCT 667

201 GluAspAlaCysSerPheGlnPheProGluGluGluArgGlyGluGlnTh 217
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668 GAGGATGCTTGCAGCTTCCAGTTCCCTGAGGAGGAACGCGGGGAGCAGAC 717
```

67 rHisCysGlyAspProGlnCysLysLysIleCysLysHisTyrProCysGlnP 84
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246 CCACTGTGCAGGACCCTCAGTGCAAGATCTGCAAGCACTACCCCTGCCAAC 295

84 roGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
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296 CAGGCCCAGAGGGTGGAGTCTCAAGGGGATATTGTGTTTGGCTTCCGGTGT 345

101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysAr 117
    |||||||||||||||||||||||||||||||||||
346 GTTGCCTGCGCCATGGGCACCTTCTCCGCAGGTCGTGACGGTCACTGCAG 395

117 gLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyA 134
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396 ACTTTGGACCAACTGTTCTCAGTTTGGATTTCTCACCATGTTCCCTGGGA 445

134 snLysThrHisAsnAlaValCysIleProLeuProThrGluGln 150
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446 ACAAGACCCACAATGCTGTGTGCATCCCGGAGCCACTGCCCACTGAGCAA 495

151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePh 167
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496 TACGGCCATTTGACTGTCATCTTCCTGGTCATGGCTGCATGCATTTTCTT 545

167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
    |||||||||||||||||||||||||||||||||||
546 CCTAACCACAGTCCAGCTCGGCCTGCACATATGGCAGCTGAGGAGGCAAC 595

184 isMetCysProArgGluThrGlnProPheAlaGlnValGlnLeuSerAla 200
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596 ACATGTGTCCTGAGAGACCCAGCCATTCGCGAGGTGCAGTTGTCAGCT 645

201 GluAspAlaCysSerPheGlnPheProGluGluGluArgGlyGluGlnTh 217
    |||||||||||||||||||||||||||||||||||
646 GAGGATGCTTGCAGCTTCCAGTTCCCTGAGGAGGAACGCGGGGAGCAGAC 695

217 rGluGluLysCysHisLeuGlyLeuGlyArgTrpPro 228
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696 AGAAGAAAAGTGTCATCTGGGGGGTCGGTGCCA 729

seq_name: N_Geneseq_34:V19152

seq_documentation_block:
ID V19152 standard; DNA; 1073 BP.
AC V19152;
DT 28-JUL-1998 (first entry)
DE Nucleotide sequence of the mouse 312C2 T cell gene.
KW Mouse 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW antigen-specific T cell proliferation; cytokine production by T-cell;
KW apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;
KW autoimmune disorders.
OS Mus sp.
FH Key   Location/Qualifiers
FT CDS   67..754
FT   /tag= a
FT   /product= "mouse 312C2 protein"
PN WO9806842-A1.
PD 19-FEB-1998.
PF 14-AUG-1997; US-027901.
PR 07-OCT-1996; US-027901.
PR 16-AUG-1996; US-689943.
PA (SCHE) SCHERING CORP.
PI Gorman DM, Randall TD, Zlotnik A;
DR WPI: 98-159534/14.
DR P-PSDB; W37838.
PT Isolated 312C2 T cell gene - used to develop products for treating,
PT e.g. cancers, auto-immune disorders, transplantation rejection and
PT other T cell disorders.
PS Claim 10; Pages 56-57; 71pp; English.
CC This is the nucleotide sequence encoding the mouse 312C2 T cell
CC protein. The 312C2 proteins are expressed in thymus cells and are
CC induced on T cells and spleen cells following activation. Engagement

217 rGluGluLysCysHisLeuGlyGlyArgTrpPro 228
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718 AGAGAAAGTGTCATCTGGGGAGGTCGGTGGCCA 751

seq_name: N_Geneseq_34:V32774

seq_documentation_block:
ID V32774 standard; cDNA; 1031 BP.
AC V32774;
DT 29-SEP-1998 (first entry)
DE Mouse GITR-B cDNA.
KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
KW GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
KW GITR-C; ds.
OS Mus sp.
FH Key   Location/Qualifiers
FT CDS   46..930
FT   /*tag= a
FT   /product= "Mouse GITR-B"
PN WO9824895-A1.
PD 11-JUN-1998.
PF 08-NOV-1997; E06252.
PR 02-DEC-1996; GB-025074.
PA (PHAA) PHARMACIA & UPJOHN SPA.
PI Riccardi C;
DR WPI; 98-333315/29.
DR P-PSDB; W49017.
PT New isolated glucocorticoid induced TNFR related polypeptide - used
PT to stimulate lymphocyte activity and cell death rescue, useful to,
PT e.g. develop products to suppress lymphocyte activity and induce
PT apoptosis
PS Claim 1; Pages 38-40; 53pp; English.
CC The present claimed sequence represents a spliced version of the
CC mouse glucocorticoid induced TNFR-family related protein (GITR)
CC cDNA (V32773). The invention also claims for the GITR-C (V32775)
CC cDNA which is another splicing variant of GITR cDNA. The GITRs are
CC claimed to be useful for stimulating lymphocyte activity and cell death
CC rescue. GITR antagonists are claimed to be useful for suppressing the
CC lymphocyte activity and for inducing apoptotic deletion. GITR cDNAs and
CC the proteins they encode are also claimed to be useful for suppressing
CC growth of tumour cells over-expressing GITR or for the treatment of
CC refractory hodgkin's disease.
SQ Sequence 1031 BP; 234 A; 272 C; 293 G; 232 T;

alignment_scores:
    Quality: 1161.50   Length: 232
    Ratio: 5.094   Gaps: 2
Percent Similarity: 98.276 Percent Identity: 97.845

alignment_block:
US-08-911-423-2 x V32774

Align seg 1/1 to: 1 to: 1031 from: 1 to: 1031

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96 CCTAGGTCAGCCGAGTGTAGTTGAGGAGCCTGGCCCTGGCAAG 145

34 aGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaPro 50
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146 TTCAGAACGGAGTGGCAACAACACTCGCTGCTGCAGCCTGTATGCTCCA 195

51 GlyGlyGluAspCysProLysProGluArgCysIleCysValThrProGluTy 67
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196 GGCAAGGAGGACTGTCCAAAGAAAGGGTGCATATGTGTCACACCTGAGTA 245

67 rHisCysGlyAspProGlnCysLysIleCysHisTyrProCysGlnP 84
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246 CCACTGTGGAGACCCTCAGTGCAAGATCTGCAAGCACTACCCTGCCAAC 295
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84 rGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
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296 CAGGCCAGAGGTGGAGTCTCAAGGGATATTGTGTTTGGCTTCCGGTGT 345

101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspIleHisCysAr 117
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346 GTTGCCTGTGCCATGGGCACCTTCTCCGCAGGTCGTGACGGTCACTGCAG 395

117 gLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyA 134
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396 ACTTTGGACCAACTGTTCAGTTGGATTTCCACCATGTTCCCTGGGA 445

134 snLysThrHisAsnAlaValCysIleProLeuProThrGluGln 150
    |||||||||||||||||||||||||||||||||||||||||||
446 ACAAGACCCACAATGCTGTGTGCATCCCGAGCCACTGCCCACTGAGCAA 495

151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePh 167
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496 TACGGCCATTTGACTGTCATCTTCCTGGTCATGGCTGCATGCATTTTCTT 545

167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
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546 CCTAACCACAGTCCAGCTCGGCCTGCACATATGGCAGCTGAGGAGGCAAC 595

184 isMetCysProArg.........Glu..ThrGlnProPheAlaGluValG 197
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596 ACATGTGTCCCCAGTTTACTACAGAGACCCAGCCATTCGCGGAGGTGC 645

197 lnLeuSerAlaGluAlaCysSerPheGlnPheProGluGluGluArg 213
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646 AGTTGTCAGCTGAGGATGCTTGCAGCTTCCAGTTCCCTGAGGAGGAACGC 695

214 GlyGluGlnThrGluGluLysCysHisLeuGlyGlyArgTrpPro 228
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seq_name: N_Geneseq_34:V32775

seq_documentation_block:
ID V32775 standard; cDNA; 1087 BP.
AC V32775;
DT 29-SEP-1998 (first entry)
DE Mouse GITR-C cDNA.
KW Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
KW GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
KW GITR-C; ds.
OS Mus sp.
FH Key   Location/Qualifiers
FT CDS   46..714
FT   /*tag= a
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PN WO9824895-A1.
PD 11-JUN-1998.
PF 08-NOV-1997; E06252.
PR 02-DEC-1996; GB-025074.
PA (PHAA) PHARMACIA & UPJOHN SPA.
PI Riccardi C;
DR WPI; 98-333315/29.
DR P-PSDB; W49018.
PT New isolated glucocorticoid induced TNFR related polypeptide - used
PT to stimulate lymphocyte activity and cell death rescue, useful to,
PT e.g. develop products to suppress lymphocyte activity and induce
PT apoptosis
PS Claim 1; Pages 42-43; 53pp; English.
CC The present claimed sequence represents a spliced version of the
CC mouse glucocorticoid induced TNFR-family related protein (GITR)
CC cDNA (V32773). The invention also claims for the GITR-B (V32774)
CC cDNA which is another splicing variant of GITR cDNA. The GITRs are
CC claimed to be useful for stimulating lymphocyte activity and cell death
CC rescue. GITR antagonists are claimed to be useful for suppressing the
CC lymphocyte activity and for inducing apoptotic deletion. GITR cDNAs and

CC the proteins they encode are also claimed to be useful for suppressing
CC growth of tumour cells over-expressing GITR or for the treatment of
CC refractory hodgkin's disease.
SQ Sequence 1087 BP; 246 A; 287 C; 310 G; 244 T;

alignment_scores:
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    Ratio: 5.088   Gaps: 2
Percent Similarity: 90.438   Percent Identity: 90.438

alignment_block:
US-08-911-423-2 x V32775   ..

Align seg 1/1 to: V32775 from: 1 to: 1087

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  1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 46 ATGGGGGCCATGGGCCATGCTGTATGGAGTCTCGATGCTCTGTGTGCTGGA 95

 17 pLeuGlyGlnProSerValValGluGluValProGlyCysGlyProGlyLysV 34
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 96 CCTAGGTCAGCCGAGTGAGTTGAGGAGCCTGGCTGTGGCCCTGGCAAGG 145

 34 aIGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrArgAlaPro 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
146 TTCAGAACGGAAGTGGCAACAACACTCGCTCGCTGAGCCTGTATGCTCCA 195

 51 GlyLysGluAspCysProLysProLysGluCysIleCysValThrProGluTy 67
    ||||||||||||||||||||||||||||||||||||||||||||||||||
196 GGCAAGGAGGACTGTCCAAAAGAAAGGTGCATATGTGTCACACCTGAGTA 245

 67 rHisCysGlyAspProGlnCysLysLysSerLysHisTyrProCysGlnP 84
    ||||||||||||||||||||||||||||||||||||||||||||||||||
246 CCACTGTGGAGACCCTCAGTGCAAGAAGTCTGCAAGCACTACCCCTGCCAAC 295

 84 roGlyGlnArgValGluSerGlnAsnGlyAspIleValPheGlyPheArgCys 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
296 CAGGCCAGAGGGTGGAGTCTCAAGGGGATATTGTGTTTGGCTTCCGGTGT 345

101 ValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysSerAr 117
    ||||||||||||||||||||||||||||||||||||||||||||||||||
346 GTTGCCTGTGCCATGGGCACCTTCTCCGCAGGTCGTGACGGTCACTGCAG 395

117 gLeuTrpThrAsnCysSerGlnProGlyPheLeuThrMetPheProGlyA 134
    ||||||||||||||||||||||||||||||||||||||||||||||||||
396 ACTTTGGACCAACTGTTCTCAGTTTGGATTTCTCACCATGTTCCCTGGGA 445

134 snLysThrHisAsnAlaValCysIleProGluProLeuProThrGluGln 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
446 ACAAGACCCACAATGCTGTGTGCATCCCGGAGCCACTGCCCACTGAGCAA 495

151 TyrGlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePh 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||
496 TACGGGCCATTGACTGTCATCTTCCTGGTCATGGCTGCATGCATTTTCTT 545

167 eLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArgGlnH 184
    ||||||||||||||||||||||||||||||||||||||||||||||||||
546 CCTAACCACAGTGCAGCTCCAGCTCCGCCTGCACATATGGCAGCTGAGGAGGCAAC 595

184 isMetCysProArg.......................... 188
    ||||||||||
596 ACATGTGTCCCCGGATGCAGTTGTGTCCCCAGGGAAGGGGAAAATGTGTCT 645

189 ..................Glu.ThrGlnProPheAlaG 195
    ||||||||||||
646 CAGGGCCCCTCACTTACCGCCCAGTTTACTACAGAGACCCCAGCCATTCGCGG 695

195 luValGlnLeuSerAlaGluAspAlaCysSerPheGlnPheProGluGlu 211
    ||||||||||||||||||||||||||||||||||
696 AGGTGCAGTTGCAGCTGAGGATGCTTGCAGCTTGCAGCTTCCCAGTTCCCTGAGGAG 745

212 GluArgArgGlyGluGlnThrGluGluLysGluLysLysLeuGlyLeuGlyArgTrpPr 228
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    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
746 GAACGCGGGGAGCAGACAGAAGAAAAGTGTCATCTGGGGGGTCGGTGCC 795

228 o 228
    |
796 A 796
```

seq_name: N_Geneseq_34:V19153

seq_documentation_block:
ID V19153 standard; DNA; 1006 BP.
AC V19153;
DT 28-JUL-1998 (first entry)
DE Nucleotide sequence of the human 312C2 T cell gene.
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW antigen-specific T cell proliferation; cytokine production by T-cell;
KW apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;
KW autoimmune disorders.
OS Homo sapiens.
FH Key   Location/Qualifiers
FT CDS   1..726
FT   /*tag= a
FT   /product= "human 312C2 protein"
PN WO9806842-A1.
PD 19-FEB-1998.
PF 14-AUG-1997; U13931.
PR 07-OCT-1996; US-027901.
PR 16-AUG-1996; US-689943.
PA (SCHE) SCHERING CORP.
PI Gorman DM, Randall TD, Zlotnik A;
DR WPI; 98-159534/14.
DR P-PSDB; W37839.
PT Isolated 312C2 T cell gene - used to develop products for treating,
PT e.g. cancers, auto-immune disorders, transplantation rejection and
PT other T cell disorders
PS Claim 10; Pages 58-59; 71pp; English.
CC This is the nucleotide sequence encoding the human 312C2 T cell
CC protein. The 312C2 proteins are expressed in thymus cells and are
CC induced on T cells and spleen cells following activation. Engagement
CC of 312C2 stimulates proliferation of T cell clones, antigen-specific
CC proliferation and cytokine production by T-cells, and potentiates T
CC cell expansion or apoptosis. The products can be used in the
CC treatment of conditions associated with abnormal physiology or
CC development, including abnormal proliferation, e.g. cancerous
CC conditions or degenerative conditions. They can be used in the
CC regulation or development of haematopoietic cells, e.g. lymphoid cells
CC which affect immunological responses, e.g. autoimmune disorders.
SQ Sequence 1006 BP; 156 A; 331 C; 337 G; 182 T;

alignment_scores:
    Quality: 660.50   Length: 235
    Ratio: 3.458   Gaps: 3
Percent Similarity: 81.277   Percent Identity: 57.021

alignment_block:
US-08-911-423-2 x V19153   ..

Align seg 1/1 to: V19153 from: 1 to: 1006

```
  1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs 17
    ||||||||  ||||||||:..||||||:.:||:||||||||:|||:::
 19 ATGGGCGGCGTTCGGGCCCTGCGGCCCTGCCGCCTCGCTGCGCGCGCTCAG 68

 17 pLeuGlyGlnProSerValValGluGluValProGlyCysGlyProGlyLysV 34
    :|||||||    ||  ::    |||||||||||:||||||||||||:::
 69 CCTGGGTCAGCGCCCC...ACCGGGGGTCCGGGTCGCGCCCCTGGGCGCC 115

 34 aIGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAla... 49
    ::  ||:||| |||:..|||||||||||:||||||:: ||||||  :
116 TCCTGCTTGGACGGACGGACGCGCTGCCGCGTTCACCGACG 165

 50 ..........ProGlyLysGluAspCysProLysProLysGluArgCy 60
    ...............
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```
PT  e.g. cancers, auto-immune disorders, transplantation rejection and
PT  other T cell disorders
PS  Disclosure; Pages 60-61; 71pp; English.
CC  This is the reverse translated nucleotide sequence of the truncated
CC  human 312C2 T cell protein from clone_A8.  The 312C2 proteins are
CC  expressed in thymus cells and are induced on T cells and spleen cells
CC  following activation.  Engagement of 312C2 stimulates proliferation
CC  of T cell clones, antigen-specific proliferation and cytokine
CC  production by T-cells, and potentiates T cell expansion or apoptosis.
CC  The products can be used in the treatment of conditions associated
CC  with abnormal physiology or development, including abnormal
CC  proliferation, e.g. cancerous conditions or degenerative conditions.
CC  They can be used in the regulation or development of haematopoietic
CC  cells, e.g. lymphoid cells which affect immunological responses, e.g.
CC  autoimmune disorders.
SQ  Sequence   723 BP;    80 A;    92 C;   163 G;    94 T;

alignment_scores:
      Quality:       509.50            Length:     236
        Ratio:        3.107              Gaps:       5
Percent Similarity:  69.492    Percent Identity:  48.729

alignment_block:
US-08-911-423-2 x V19154

Align seg 1/1   to: V19154   from: 1 to: 723

  1 MetGlyAlaTrpAlaMetLeuTyrGlyValSerMetLeuCysValLeuAs  17
    |||||||||                     :|||    |:|||
 19 ATGGGNGCNTTYMGNGCNYTNTGYGGNYTNGCNYTNTNTGYGCNYTNWS  68

 17 pLeuGlyGlnProSerValValGluGluProGlyIleCysGlyProGlyLysV  34
    :|||                  ::           ||||||||||||||
 69 NYTNGGNCARMGNCCN..ACNGGNGGNCCNGGNTGYGGNCCNGGNMGNY  115

 34 aIleGlnAsnGlySerGlyAsnAsnThrArgCysCysSerLeuTyrAla...  49
    |||:|||:||::::::      |||||:|||::|
116 TNYTNYTNGGNACNGGNACNGAYGCNMGNTGYTGYMGNTNCAYACNACN  165

 50 .............ProGlyLysGluAspCysProLysGluArg..  59
                 |||||   |:|||     ||:::|||
166 MGNTGYTGYMGNGAYTAYCCNGGN...GARGARTGYTGYWSNGARTGGGA  212

 60 .CysIleCysValThrProGluTyrHisCysGlyAspProGlnCysLysI  76
    :||||    ||:|||||:::|||||||||||||:::|||:::
213 YTGYATGYGYGTNACARCCNGARTTYCAYTGYGGNGAYCCNTGYACNA  262

 76 leCysLysHisTyrProCysGlnProGlyIleArgValGluSerGlnGly  92
    :|||    ||||||:||||:|||||||||||||:::|||
263 CNTGYMGNCAYCAYCCNTGYCCNCCNGGNCARGGNTNCARWSNCARGGN  312

 93 AspIleValPheGlyPheArgCysValAlaCysAlaMetGlyThrPheSe  109
    :::     ||||||||:::|||||||:::|||:||||||
313 AARTTYWSNTTYGGNTTYCARTGYATHGAYTGYGCNWSNGGNACNTTYWS  362

109 rAlaGlyAspGlyHisCysArgLeuTrpThrAsnCysSerGlnPheG  126
    :::|||||||:::||||||||:||||:::|||:||:|||
363 NGGNGGNCAYGARGGNCAYTGYAARCCNTGGACNGAYTGYACNCARTTYG  412

126 lyPheLeuThrMetPheProGlyAsnLysThrHisAsnAlaValCysIle  142
    ||||    |||:::|||||||||||||||||:::|||
413 GNTTYYTNACNGTNTTYCCNGGNAAYAARACNCAYAAYGCNGTNTGYGTN  462

143 ProGluProLeuProThrGluGlnTyrGlyHisLeuThrValIlePheLe  159
    |||    ||::||||||:::|||||||||:::
463 CCNGGNWSNCCNCCNGGNCARCCNYTNGGNTGGGTNACNGTNGTNNTYNT  512

159 uValMetAlaAlaCysIlePhePheLeuThrThrValGlnLeuGlyLeuH  176
    :::|||||:::||||||||     |||    |||
513 NGCNGTNGCNGCNTGYGTNGTNTNTNTNTNACNWSNGCNCARYTNGGNYTNC  562

176 isIleTrpGlnLeuArgArgGlnHisMetCysProArgGluThrGlnPro  192
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166 CGCTGCTGCCCGATTACCCGGGCCGAGGAGTGCTGTTCCGAGTGGGACTG  215
    ||||||                   ||   |||    ||:::
 60 sIleCysValThrProGluTyrHisCysGlyAspProGlnCysLysIleC  77
    |:::||||   ||||||:::||||||||||||   ||:::|
216 CATGTGTGTCACAGCCYGAARTTCCACTGCGGAGACCCTTGCTGCACGACCT  265

 77 ysLysHisTyrProCysGlnProGlyIleArgValGluSerGlnGlyAsp  93
    ||:::||||||   ||||:|||||||||||   ||:::|||
266 GCCGGCACCACCCTTGTCCCCAGGCCAGGGGTACAGTCCCAGGGAAA  315

 94 IleValPheGlyPheArgCysValAlaCysAlaMetGlyThrPheSerAl  110
    :||||||||||:::|||||||:::|||:|||||   ||:::
316 TTCAGTTTGGCTTCCAGTGATCGACTGTGCCCTGGGGACCTTCTCCGG  365

110 aGlyArgAspGlyHisCysArgLeuTrpThrAsnCysSerGlnPheGlyP  127
    :||:::|||||||:::||||||||:||||:::|||:||
366 GGGCCACGAAGGCCACTGCAAACCTTGGACAGACTGCACCCAGTTCGGGT  415

127 heLeuThrMetPheProGlyAsnLysThrHisAsnAlaValCysIlePro  143
    ||||   |||:::|||||||||||||||||:::|||
416 TTCTCACTGTTTCCCTGGGAACAAGACCCACAACCCTGTGCGTCCCA  465

144 GluProLeuProThrGluGlnTyrGlyHisLeuThrValIlePheLeuVa  160
    |||   ||::|||||||:::|||||||||:::
466 GGGTCCCCGCCGGCAGAGCCGCTTGGGTGGGCTGACCGTGTCCTGGC  515

160 lMetAlaAlaCysIlePhePheLeuThrThrValGlnLeuGlyLeuHisI  177
    :::|||||:::||||||||   |||   |||
516 CGTGGCCGCGTCCGTCCTCCTGGACTGGACTGCACA  565

177 leTrpGlnLeuArgArgGlnHisMetCysProArgGluThrGlnProPhe  193
    ||||||||||||   |||||:|||||||   :::
566 TCTGGCAGTTGAGGAGTCACGTGGCCCAGAGACCCAGCTGCTG  615

194 AlaGluValGlnLeuSerAlaGlnAspAlaCysSerPheGlnPheProGl  210
    ||||||||:::|||    :||||||   ||||||   :::
616 CTGGAGGTGCCCGCTGCGACCCGCAAGACGCCAGAAGCTGCCAGTTCCCCGA  665

210 uGluGluArgGlyGluGln...ThrGluLeuLysCysHisLeuGlyGlyA  226
    :||||||||:::|||         :||||||||:::|||
666 GGAAGAGCGGGCGGGCGAGCGATCGGCAGAGGAGAAGGGGCGGCTGGGAGACC  715

226 rgTrp  227
    |||
716 TGTGG  720
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seq_name: N_Geneseq_34:V19154

documentation_block:
     V19154 standard; DNA; 723 BP.
AC   V19154;
DT   28-JUL-1998  (first entry)
DE   Truncated human 312C2 protein from clone_A8 nucleotide sequence.
KW   Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW   antigen-specific T cell proliferation; cytokine production by T-cell;
KW   apoptosis; cancer; haematopoietic cells; lymphoid cell; ss;
KW   autoimmune disorders.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   CDS            1..723
FT                  /*tag= a
FT                  /product= "truncated human 312C2 protein from clone_A8"
PN   WO9806842-A1.
PD   19-FEB-1998.
PF   14-AUG-1997; U13931.
PR   07-OCT-1996; US-027901.
PR   16-AUG-1996; US-689943.
PA   (SCHE ) SCHERING CORP.
PI   Gorman DM, Randall TD, Zlotnik A;
DR   WPI; 98-159534/14.
DR   P-PSDB: W37840.
PT   Isolated 312C2 T cell gene - used to develop products for treating,
```

```
        |||||||||||         |||   |||   |||   |||||||||
    563 AYATHTGGCARYTNMGNWSNCARTGYATGTGGCCNMGNGARACNCARYTN 612

    193 PheAlaGluValGlnLeuSerAlaGluAspAlaCysSerPheGlnPhePr 209
              ||||||:::   ::::::|||||||||   :::   ||||||||
    613 YTNYTNGARGTNCCNCCNWSNACNGARGAYGCNMGNWSNTGYCARTTYCC 662

    209 oGluGluGluArgGlyGlu...GlnThrGluGluLysCysHisLeuGlyG 225
        ||||||||||   ||||||      :::|||||||||         |||:
    663 NGARGARGARMGNGGNGARMGNWSNGCNGARGARAARGGNMGNYTNGGNG 712

    225 lyArgTrp 227
        ::   |||
    713 AYYTNTGG 720

seq_name: N_Geneseq_34:Q86126

seq_documentation_block:
     Q86126 standard; cDNA; 838 BP.
     Q86126;
DT   16-OCT-1995  (first entry)
DE   H4-1BB receptor protein cDNA.
KW   H4-1BB; receptor protein; immunosuppressive; autoimmune disease;
KW   organ transplantation; cell membrane ligand; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             41. .808
FT                   /*tag=  a
PN   WO9507984-A.
PD   23-MAR-1995.
PF   15-SEP-1994; U10457.
PR   16-SEP-1993; US-122796.
PA   (INDV ) UNIV INDIANA FOUND.
PI   Kwon BS;
DR   WPI; 95-131352/17.
DR   P-PSDB; R70977.
PT   Novel cDNA encoding human receptor protein H4-1BB - useful to
PT   produce the protein which is used to treat auto:immune disease
PT   and facilitate organ transplantation
PS   Claim 2; Fig.2; 36pp; English.
CC   Human peripheral blood lymphocyte-derived cDNA was amplified by PCR
CC   using probes based on the mouse receptor protein 4-1BB gene.  The PCR
CC   product was used to screen a cDNA library of activated human T-cells.
CC   The isolated cDNA (Q86126), deposited as NRRL B21131, encoded the
CC   human homolog, H4-1BB (R70977), of 4-1BB.
SQ   Sequence   838 BP;    218 A;    191 C;    215 G;    214 T;

 ignment_scores:
          Quality:  176.00           Length:    269
            Ratio:  1.313              Gaps:     16
 Percent Similarity:  49.814   Percent Identity: 26.022

alignment_block:
 US-08-911-423-2 x Q86126   ..

 Align seg 1/1  to: Q86126  from: 1  to: 838

     11 SerMetLeuCysValLeuAspLeuGlyGlnProSerValValGluGluPr 27
        ::::::|||   ||||||::::::   ::::::      :::::::::||
     71 ACTCTGTTGCTGGTCCTCAACTTTGAGAGGACAAGATCATTGCAGGATCC 120

     27 o................................................. 27
        |
    121 TTGTAGTAACTGCCCAGCTGGTACATTCTGTGATAATAACAGGAATCAGA 170

     28 ........GlyCysGlyProGlyLysValGlnAsnGlySerGlyAsnAsn 41
                   |||   |||:::         :::::::::|||:::
    171 TTTGCAGTCCCTGTCCTCCAAATAGTTTCTCCAGCGCAGGTGGACAAAGG 220

     42 Thr...............ArgCysCysSerLeuTyrAlaProGlyLysGl 53
        |||               :::|||   :::::::::         :::
    221 ACCTGTGACATATGCAGGCAGTGTAAAGGTGTTTTC...AGGACCAGGAA 267
```

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  53 uAspCys.........ProLysGluArgCysIleCysValThrProGluT 67
      :::|||         :::::::::   |||   |||   ||||||   :
 268 GGAGTGTTCCTCCACCAGCAATGCAGAGTGTGACTGC...ACTCCAGGGT 314

  67 yrHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGln 83
     ::||||||   ::::::   |||   :::|||   :::      |||:::
 315 TTCACTGCCTGGGGGCAGGATGCAGCATGTGTGAACAG...GATTGTAAA 361

  84 ProGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCy 100
     :::||||||   :::      :::|||                     ||
 362 CAAGGTCAAGAACTGACAAAAAAAGGT.....................TG 390

 100 sValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysA 117
     |   :::|||    |||||||||||::::::   :::   |||   ||||
 391 TAAAGACTGTTGCTTTGGGACATTTAACGATGAGAAACGTGGCATCTGTC 440

 117 rgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGly 133
     ||   |||||||||||||||      |||      ::::::      |||
 441 GACCCTGGACAAACTGTTCTTTGGATGGAAAGTCTGTGCTTGTGAATGGG 490

 134 AsnLysThrHisAsnAlaValCys.......................... 141
     :::|||   :::::::::||||||
 491 ACGAAGGAGAGGGACGTGGTCTGTGGACCATCTCCAGCTGACCTCTCTCC 540

 142 ............IleProGluProLeuProThrGluGlnTyrGlyHis. 153
                  ::::::   |||   |||:::   :::   ||||||
 541 GGGAGCATCCTCTGTGACCCCGCCTGCCCCTGCGAGAGAGCCAGGACACT 590

 154 ........LeuThrValIlePheLeuValMetAlaAlaCys......... 164
             ::::::  ||||||||||::::::::::::
 591 CTCCGCAGATCATCTCCTTCTTTCTTGCGCTGACGTCGACTGCGTTGCTC 640

 165 ......IlePhePheLeuThrThrValGlnLeuGlyLeuHisIleTrpGl 179
           :::||||||||||||               |||::::::
 641 TTCCTGCTGTTCTTCCTCACG...............CTCCGTTTCTCTGT 675

 179 nLeuArgArgGlnHisMetCysProArgGlu..................T 190
      ::::::|||               |||                     :
 676 TGTTAAACGG............GGCAGAAAGAAACTCCTGTATATATTCA 713

 190 hrGlnProPheAla...GluValGlnLeuSer...AlaGluAspAlaCys 204
     ::|||||||||         ||||||   :::   :::||||||:::|||
 714 AACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATGGCTGT 763

 205 SerPheGlnPheProGluGluGluArgGlyGluGlnThrGluGluLysCy 221
     ||| ::::||||||||||||||||:              |||      ||
 764 AGCTGCCGATTTCCAGAAGAAGAA...............GAAGGAGGATG 798

 221 sHisLeu 223
     |:::|||
 799 TGAACTG 805

seq_name: N_Geneseq_34:Q75424

seq_documentation_block:
ID   Q75424 standard; cDNA to mRNA; 1415 BP.
AC   Q75424;
DT   08-AUG-1995  (first entry)
DE   Human 4-1BB polypeptide coding sequence.
KW   T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW   proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             120. .887
FT                   /*tag=  a
FT                   /product= 4-1BB polypeptide.
FT   signal_peptide  120. .188
FT                   /*tag=  b
FT   mat_peptide     189. .884
FT                   /*tag=  c
PN   WO9426290-A.
PD   24-NOV-1994.
```

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PF  06-MAY-1994; U05036.
PR  07-MAY-1993; US-060843.
PA  (IMMV ) IMMUNEX CORP.
PI  Alderson MR, Goodwin RG, Smith CA;
DR  WPI; 95-022265/03.
DR  P-PSDB; R6419?.
PT  Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor
PT  4-1BB to transduce signal
PS  Claim 29; Page 46-47; 65pp; English.
CC  The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see
CC  Q75423) are useful in a pharmaceutical composition for stimulating
CC  the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful
CC  for exploring mechanisms of T-cell activation, as they are expressed
CC  on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for
CC  in vitro cultivation of primary T-cells during the derivation of
CC  clonal T-cell lines.  It may also be used to stimulate proliferation
CC  of activated T-cells, used in therapeutic procedures.
SQ  Sequence  1415 BP;  385 A;  332 C;  333 G;  365 T;

alignment_scores:
        Quality:  176.00        Length:      269
        Ratio:    1.313         Gaps:         16
Percent Similarity: 49.814      Percent Identity: 26.022

alignment_block:
US-08-911-423-2 x Q75424

Align seg 1/1  to: Q75424  from: 1  to: 1415

  11 SerMetLeuCysValLeuAspLeuGlyGlnProSerValValGluPr  27
     ::::::|||  ||||||:::::  :::::  ::::::::::||
 150 ACTCTGTTCGCTGGTCCCTCAACTTTGAGAGGACAAGATCATTGCAGGATCC 199

 -27 o..........................................  27
     |
 200 TTGTAGTAACTGCCCAGCTGGTACATTCTGTGATAATAACAGGAATCAGA 249

  28 ........GlyCysGlyProGlyLysValGlnSerGlyAsnAsn  41
     ||| |||:||  :::::  |||:||
 250 TTTGCAGTCCCTGTCCTCCAAATAGTTCTCCAGCCGCAGGTGGACAAAGG 299

  42 Thr.............ArgCysCysSerLeuTyrAlaProGlyLysGl  53
     |||             :::||||  :::::::::
 300 ACCTGTGACATATGCAGGCAGTGTAAAGGTGTTTTC..AGGACCAGGAA 346

  53 uAspCys...........ProLysGluArgCysIleCysValThrProGluT  67
     :::||           ::::::: ||| ||||||  |||||| :
 347 GGAGTGTTCTCCACCAGCAATGCAGAGTGACTGC..ACTCCAGGGT 393

  67 yrHisCysGlyAspProGlnCysLysIleCysLysHisTyrProCysGln  83
     ::||||  ::::  ||||||  ::: ||| :  :::
 394 TTCACTGCCTGGGGCCAGGATGCAGCAGCATGTGAACAG...GATTGTAAA 440

  84 ProGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCy 100
     ::|||||  ::::::::  ::||
 441 CAAGGTCAAGAAACTGACAAAAAAGGT...............TG 469

 100 sValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysA 117
     ::|||  ||||||||:::::::  :::  ||| |||
 470 TAAAGACGTTGCTTGGGACATTTAACGATCAGAAAACGTGGCCATCTGTC 519

 117 rgLeuTrpHisAsnCysSerGlnPheGlyPheLeuThrMetPheProGly 133
     :| ||||||||:::|| |||||  :::: |||
 520 GACCCTGGACAAACTGTTCTTTGGATGGAAAGTCTGTGCTTGTGAATGGG 569

 134 AsnLysThrHisAsnAlaValCys.................. 141
     :: ||  |||||:::|| :
 570 ACGAAGGAGAGGACGTGGTCTGTGGACCATCTCCAGCCGACCTCTCTCC 619

 142 ........IleProGluProLeuProThrGluGlnTyrGlyHis. 153
     ::::::  ||| |||:  ::: ||||||
 620 GGGAGCCATCTCGTGACCCCGCCCCTGCCCCTGGCCGAGAGCCAGGACACT 669
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```
 154 ......LeuThrValIlePheLeuValMetAlaAlaCys........... 164
      :::::  |||:|||||||||::|||||:
 670 CTCCGCAGATCATCCTCCTTCTTCTTCTGCCTGACGTCGACTGCCGGTGCTC 719

 165 ......IlePhePheLeuThrThrValGlnLeuGlyLeuHisIleTrpGl 179
      :::::||||||||                      |||:||:
 720 TTCCTGCTGTTCTTCCTCACG............CTCCGTTCTCTCTGT 754

 179 nLeuArgArgGlnHisMetCysProArgGlu....................T 190
     ::::||||                     |||
 755 TGTTAAACGG..................GGCAGAAGAAACTCCTGTATATTCA 792

 190 hrGlnProPheAla...GluValGlnLeuSer...AlaGluAspAlaCys 204
     ::|||||||       ||||||  ::: :::||||||:::|||
 793 AACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATGGCTGT 842

 205 SerPheGlnPheProGluGluGluArgGlyGlyGluGlnThrGluGluLysCy 221
     |||  |||||||||||||                 ||
 843 AGCTGCCGATTTCCAGAAGAAGAA.............GAAGGAGGATG 877

 221 sHisLeu 223
     |:::|||
 878 TGAACTG 884


seq_name: N_Geneseq_34:T91026

seq_documentation_block:
ID  T91026 standard; cDNA to mRNA; 1415 BP.
AC  T91026;
DT  25-FEB-1998  (first entry)
DE  Human 4-1BB receptor cDNA clone hu4-1BB.
KW  4-1BB ligand; 4-1BB-L; receptor; human; cytokine; T lymphocyte;
KW  T cell; proliferation; immunostimulant; ss.
OS  Homo sapiens.
FH  Key              Location/Qualifiers
FT  CDS              120..887
FT                   /*tag= a
FT  sig_peptide      120..188
FT                   /*tag= b
FT  mat_peptide      189..884
FT                   /*tag= c
PN  US5674704-A.
PD  07-OCT-1997.
PF  07-MAY-1993; 060843.
PR  06-MAY-1994; US-236918.
PR  07-MAY-1993; US-060843.
PA  (IMMV ) IMMUNEX CORP.
PI  Alderson MR, Goodwin RG,  Smith CA;
DR  WPI; 97-502333/46.
DR  P-PSDB; W26658.
PT  DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating
PT  T-cell proliferation in vitro, and as research tools
PS  Example 2; Column 43-46; 32pp; English.
CC  This cDNA clone encodes human 4-1BB (see W26658), a member of the
CC  tumour necrosis factor receptor superfamily that is expressed on
CC  cells that include, but are not limited to, stimulated human
CC  peripheral blood lymphocytes.  The clone was isolated from a cDNA
CC  library prepared from human peripheral blood T-lymphocytes that
CC  had been activated with phytohaemagglutinin and phorbol myristate
CC  acetate.  A fragment of murine 4-1BB DNA (see T91027) was used
CC  as probe.  A novel claimed cytokine, designated 4-1BB ligand
CC  (4-1BB-L) has been identified, cloned and sequenced (see W26657)
CC  that binds to 4-1BB.  4-1BB-L, especially its soluble extracellular
CC  domain, can be used to stimulate T-cell proliferation in vitro, as
CC  a research tool and as an affinity ligand for purifying 4-1BB.
SQ  Sequence  1415 BP;  385 A;  332 C;  333 G;  365 T;

alignment_scores:
        Quality:  176.00        Length:      269
        Ratio:    1.313         Gaps:         16
Percent Similarity: 49.814      Percent Identity: 26.022
```

seq_name: N_Geneseq_34:T88969

```
seq_documentation_block:
ID   T88969 standard; DNA; 946 BP.
AC   T88969;
DT   01-APR-1998  (first entry)
DE   DNA encoding a human h4-1BBSV receptor.
KW*  h4-1BBSV receptor; 4-1BB receptor splicing variant; endotoxic shock;
KW   tumour necrosis factor; TNF ligand; T-cell activation; inflammation;
KW   tumour prevention; viral infection; autoimmune disease;
KW   cellular proliferation; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             124..783
FT                   /*tag= a
FT   sig_peptide     124..177
FT                   /*tag= b
FT                   /note= "putative"
FT   mat_peptide     178..780
FT                   /*tag= c
PN   WO9733898-A1.
PD   18-SEP-1997.
PF   15-MAR-1996;  U03587.
PR   15-MAR-1996;  WO-U03587.
PA   (HUMA-) HUMAN GENOME SCI INC.
PI   Gentz RL, Ni J, Yu G;
DR   WPI; 97-470806/43.
DR   P-PSDB; W31759.
PT   Human 4-1BB receptor splicing variant and related DNA - used to
PT   develop products for treating e.g. tumours, viral infection,
PT   endotoxic chock, autoimmune disease or bone resorption.
PS   Claim 8; Fig 1; 73pp; English.
CC   The present sequence encodes a novel human h4-1BBSV receptor. This is a
CC   human 4-1BB receptor splicing variant. The 4-1BB ligand is a member of
CC   the tumour necrosis factor (TNF) family of ligands. It is induced by
CC   T-cell activation. The h4-1BBSV receptor nucleic acid and protein can be
CC   used for diagnosis and therapy. In particular, agonists of h4-1BBSV
CC   receptor can be used to treat and/or prevent tumours, restenosis,
CC   cytotoxicity, bacterial and viral infection, deleterious effects of
CC   ionising radiation, autoimmune disease, AIDS and graft-host rejection,
CC   to regulate immune responses, wound healing and cellular proliferation.
CC   Antagonists can be used to treat and/or prevent endotoxic shock,
CC   inflammation, cerebral malaria, activation of the HIV virus, graft
CC   rejection, bone resorption and cachexia.
SQ   Sequence   946 BP;   257 A;   218 C;   230 G;   241 T;
```

```
alignment_scores:
         Quality:   174.00              Length:        249
         Ratio:      1.381              Gaps:           15
Percent Similarity:  50.602    Percent Identity:    27.309

alignment_block:
US-08-911-423-2 x T88969

Align seg 1/1  to: T88969   from: 1  to: 946

     11 SerMetLeuCysValLeuAspLeuGlyGlnProSerValValGluGluPr  27
        ::::::|||  |||||||:::::  :::::   ::::::::::|
    154 ACTCTGTTCGTGGTCCTCAACTTTGAGAGGACAACAGATCATTGCAGGATCC  203

     27 oGlyCysGlyProGlyLysValGlnAsnGlySerGlyAsnAsnThrArgC    44
        | !||||||
    204 T.....                                               204

     44 ysCysSerLeuTyrAlaProGly............         LysGluAspCys...  55
        |||||                                      ::  :||
    205 ..TGTAGTAACTGCCCAGCTGGTGTTTCAGGACCAGGAAGGAGTGTTCC   252

     56 .....ProLysGluArgCysIleCysValThrProGluTyrHisCysGl    70
        ||||||  ||| |||||||  ::||||| ::|||||||
    253 TCCACCAGCAATGCAATGCAGAGTGTGACTGC..ACTCCAGGGTTCACTGCCT   299
```

```
PS   Disclosure; Page 36-37; 48pp; English.
CC   A cDNA clone (T39546) codes for novel human receptor protein
CC   H4-1BB (W04174), a protein that has the potential to function as
CC   an accessory signaling molecule during T-cell activation and
CC   proliferation.  The cDNA clone was isolated from a lambda gt11
CC   cDNA library of activated human T lymphocytes by screening with a
CC   PCR product obtd. by amplification of lymphocyte cDNA using
CC   primers (see also T39542-45) based on the murine 4-1BB cDNA
CC   (T39541).    It can be used to produce recombinant H4-1BB useful
CC   for isolating H4-1BB ligands, for stimulating proliferation of
CC   B-cells expressing H4-1BB ligands, for blocking H4-1BB ligand
CC   binding and for raising anti H4-1BB monoclonal antibody.
SQ   Sequence  838 BP;    218 A;    192 C;    214 G;    214 T;

alignment_scores:
     Quality:    157.00               Length:    269
     Ratio:      1.180                Gaps:      16
Percent Similarity:  49.442   Percent Identity: 25.651

alignment_block:
US-08-911-423-2 x T39546

Align seq 1/1 to: T39546    from: 1  to: 838
```

```
 70 yAspProGlnCysIleCysLysLysTyrProCysGlyGlnA  87       11 SerMetLeuCysValLeuAspLeuGlyGlnProSerValValGluGluPr  27
    :::::   |||    ::|||     |||:::::||||||                 ::::::||| |||||| ::::::  ::::::  :::::::||
300 GGGGGCAGGATGCAGCATGTGAACAG...GATTGTAAACAAGGTCAAG 346      71 ACTCTGTTGCTGGTCCTCAACTTTGAGAGGACAAGATCATTGCAGGATCC 120

 87 rgValGluSerGlnGlyAspIleValPheGlyPheArgCysValAlaCys 103       27 o.................................................  27
    ::  :::|||                      ||| :::|||                  -
347 AACTGACAAAAAAGGT..................TGTAAAGACTGT 375      121 TTGTAGTAACTGCCCAGCTGGTACATTCTGTGATAATAACAGGAATCAGA 170

104 AlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysArgLeuTrpTh 120       28 .....GlyCysGlyGlyLysLysValGlnAsnGlySerGlyAsnAsn  41
    ||||||||:::::  ::|  ||| |||||  |||||                       |||  :::::::|||:::
376 TGCTTTGGGACATTAACGATCAGAAACGTGGCATCTGTCGACCCTGGAC 425      171 TTTGCAGTCCCTGTCCTCCAAATAGTTTCTCCAGCGCAGGTGGACAAAGG 220

120 rAsnCysSerGlnPheGlyPheLeuThrMetPheProGlyAsnLysThrH 137       42 Thr............ArgCysSerSerLeuTyrAlaProGlyLysGl  53
    ||||||||||        |||   ::::|||                            |||            ::::||
426 AAACTGTTCTTTGGATGGAAAGTCTGTGCTTGTGAATGGGACGAAGGAGA 475      221 ACCTGTGACATATGCAGGCAGCGAGTGTAAAGGTGTTTC...AGGACCAGGAA 267

137 isAsnAlaValCys.......................... 141               53 uAspCys...........ProLysGluArgCysIleCysValThrProGluT  67
    :::::|||:::||||||                                          ::::||            |||||:::|||||||
476 GGGACCTGGTCTGTGACCACCATCTTCAGCCGACCTCTCCGGGAGCATCC 525      268 GGAGTGTTCCTCACCAGCACAGCAGGTGGACTGC...ACTCCAGGGT 314

142 ...IleProGluProThrGlyGlnTyrGlyHis........Le 154               67 yrHisCysGlyAspProGlnCysLysLysIleCysLysLysTyrProCysGln  83
    ::: ||| ||||:: :::  |||||                                  :::::||||||||||||||||||||||      ||||
526 TCTGTGACCCCGCCCTGCCCCTGCGAGAGCCAGGACACTCTCCGCAGAT 575      315 TTCACTGCCTGGGGCAGGATGCAGCATGTGAACAG...GATTGTAAA 361

154 uThrValIlePheLeuValMetAlaAlaCys.................IleP 166       84 ProGlyGlnArgValGluSerGlnGlyAspIleValPheGlyPheArgCys 100
    ::|||  ||||:::||||||:::::::||||                            ::::||||||  :::                :::|||
576 CATCTCCTTCTTTCTTGGCGATCGCGACGTCGACTGCTTCTTCCTGCTGT 625      362 CAAGGTCAAGAACTGACAAAAAAGGT.................TG 390

166 hePheLeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgArg 182      100 sValAlaCysAlaMetGlyThrPheSerAlaGlyArgAspGlyHisCysA 117
    ||||||||     |||||  ::: :::|||                             :::|||  ||||||||:::::  ::|  ||| |||||
626 TCTTCCTCACG...................CTCCGTTTCTCTGTTGTTAAACGG 660      391 TAAAGACTGTTGCTTTGGGACATTAACGATCAGAAACGTGGCATCTGTC 440

183 GlnHisMetCysProArgGlu...............ThrGlnProPh 193      117 rgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGly 133
    |||      ::|||||||||                                       ||  ||||||||||||       |||   :::|||
661 ..............GGCAGAAAGAAACTCCTGTATATATTCAAACAACCATT 698      441 GACCCTGGACAAACTGTTCTTTGGATGGAAAGTCTGTGCTTGTGAATGGG 490

193 eAla...GluValGlnLeuSer..AlaGluAspAlaCysSerPheGlnP 208      134 AsnLysThrHisAsnAlaValCys......................... 141
    ||||| ::: ::::|||||||:::||||  :::|||                       :::||    :::::|||:::||||||
699 TATGAGACACGTACAAACTACTCAAGGAGAGATGGCTGTAGCTGCCGAT 748      491 ACGAAGGAGGAGGGGACCTGGTCTGTGACCACCATCTTCAGCCGACCTCTCC 540

208 heProGluGluGluArgGlyGluGlnThrGluGlnGluLysCysHisLeu 223      142 .........IleProGluProThrGlyGlnTyrGlyHis... 153
    ||||||||     |||   ::::|||||||||                           ::: ||| ||||:: :::  |||||
749 TTCCAGAGAAGAA..............GAAGGAGGATGTGAACTG 780      541 GGGAGCATCCTCTGTGACCCCGCCCTGCCCCTGCGAGAGCCAGGACACT 590

                                                                154 ........LeuThrValIlePheLeuValMetAlaAlaCys........ 164
                                                                    ::|||  ||||:::||||||
                                                                591 CTCCGCAGATCATCTCCTTCTTTCTTGGCGATCGCGACGTCGACTGCTTGCTC 640
```

```
seq_name: N_Geneseq_34:T39546

seq_documentation_block:
    T39546 standard: cDNA to mRNA; 838 BP.
PN  T39546: (first entry)
    12-DEC-1996
DE  Human receptor H4-1BB cDNA.
KW  Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW  immunostimulant; cancer; autoimmune disease; graft rejection;
KW  therapy; ss.
OS  Homo sapiens.
FH  Key          Location/Qualifiers
FT  cds          41..808
FT               /*tag= a
FT  mat_peptide  41..805
FT               /*tag= b
PN  WO629348-A1.
PD  26-SEP-1996.
PF  22-MAR-1996; U03965.
PR  23-MAR-1995; US-409851.
PA  (INDV) UNIV INDIANA FOUND.
PI  Kang C, Kwon BS;
DR  WPI; 96-43138/44.
DR  P-PSDB: W04174.
PT  Monoclonal antibody specific for human receptor protein 4-1BB - used
PT  to enhance proliferation and activation of T-cells for treatment of
PT  cancer and to inhibit specific ligand binding for treating
PT  auto:immune diseases
```

```
165  .....IlePhePheLeuThrThrValGlnLeuGlyLeuHisIleTrpGl 179
641  TTCCTGCTGTTCTTCCTCACG............CTCCGTTTCTCTGT 675

179  nLeuArgArgGlnHisMetCysProArgGlu.................T 190
676  TGTTAAACGG.........GGCAGAAAGAAACTCCTGTATATATTCA 713

190  hrGlnProPheAla...GluValGlnLeuSer...AlaGluAspAlaCys 204
714  AACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATGGCTGT 763

205  SerPheGlnPheProGluGluGluArgGlyGlyGluGlnThrGluGluLysCy 221
764  AGCTGCCGATTTCCAGAAGAAGAA..........GAAGGAGGATG 798

221  sHisLeu 223
799  TGAACTG 805
```

Seq_name: N_Geneseq_34:Q92086

```
seq_documentation_block:
ID   Q92086 standard; DNA; 1439 BP.
AC   Q92086;
DT   28-MAR-1995.
PN   CA2108401-A.
PD   28-MAR-1995.
PF   14-OCT-1993; 108401.
PR   27-SEP-1993; US-127693.
PA   (REGC ) UNIV CALIFORNIA.
PI   Lotz M, Schwarz H;
DR   WPI; 95-194420/26.
DR   P-PSDB; R74087.
OS   Homo sapiens.
DE   Human receptor induced by lymphocyte activation (ILA) DNA.
KW   ILA; receptor inducible by lymphocyte activation; disease diagnosis;
KW   antiinflammatory; ss.
PT   New receptor inducible by lymphocyte activation - used to develop
PT   prods. for the diagnosis and treatment of inflammatory host defence
PT   pathology.
PS   Claim 52; Page 61; 91pp; English.
CC   This DNA may be expressed recombinantly for the production of ILA.
CC   The cDNA was isolated from a library constructed from activated
CC   human T-lymphocyte leukemia virus type-1 transformed human T-
CC   lymphocytes.
SQ   Sequence 1439 BP; 393 A; 336 C; 346 G; 364 T;
```

```
alignment_scores:
       Quality: 158.00              Length:        269
         Ratio:   1.188              Gaps:         16
Percent Similarity: 49.442      Percent Identity: 25.279
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```
alignment_block:
US-08-911-423-2 x Q92086

Align seg 1/1  to: Q92086  from: 1  to: 1439

 11  SerMetLeuCysValLeuAspLeuGlyLeuProSerValValGluGluPr 27
170  ACTCTGTTGCTGTCCCAACTTTGAGAGGACAAGATCATTGCAGGATCC 219

 27  o.................................................. 27
220  TTGTAGTAACTGCCCAGCTGGTACATTCTGTGATAATAACAGGAATCAGA 269

 28  ......GlyCysGlyProGlyLysValGlnGlnAsnGlySerGlyAsnAsn 41
270  TTTGCAGTCCCTGTCCTCCAAATAGTTTCTCCAGCCGCCGGTGGACAAAGG 319
```

```
 42  Thr................................................. 53
320  ACCTGTGACATGGAGGCAGTGTGTAAAGGTGTTTTTC...AGGACCAGGAA 366

 53  uAspCys........ProLysGluArgCysIleCysValThrProGluT 67
367  GGAGTGTTCCTCCACCAGCAATGCAGAGTGTGACTGC...ACTCCAGGGT 413

 67  yrHisCysGlyAspProGlnCysLysHisTyrProCysGln 83
414  TTCAGTGGCTGGGGCAGGATGCACATGTGAACAG...GATTGTAGA 460

 84  ProGlyGlnArgValGluSerGlnGlyAspIleValPheGlyValPheArgCy 100
461  CAAGTCAAGAACTGACAAAAAAAGT..................TG 489

100  sValAlaCysAlaMetGlyThrPheSerAlaGlyHisArgAspGlyHisCysA 117
490  TAAAGACGTTGCTTGGGACATTTAACGATCAGAAAACGTGGCATCTGTC 539

117  rgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGly 133
540  GACCCTGGACAAACTGTTCTTTGGATGGAAAGTCTGTGCCTTGTGAATGGG 589

134  AsnLysThrHisAsnAlaValCys........................... 141
590  ACGAAGGAGGACGTGGTCTGTGACCATCTCCAGCGACCTCCTCTCC 639

142  ......ThePheGluProThrGluGlnTyrGlyHis. 153
640  GGGAGCATCTCTGTGACGCCGCTGCCCTGCCGAGAGAGCCAGGACACT 689

154  ......LeuThrValIlePheLeuValMetAlaAlaCys........... 164
690  CTCCCGAGATCATCTCCTTCTTCCTTGCGGTGACGTGCGACTGCGTTGCTC 739

165  ......IlePheLeuThrThrValGlnLeuGlyLeuHisIleTrpGl 179
740  TTCCTGCTGTTCTTCCTCACG.........CTCCGTTTCTCTGT 774

179  nLeuArgArgGlnHisMetCysProArgGlu.................T 190
775  TGTTAAACGG.........GGCAGAAAGAAACTCCTGTATATATTCA 812

190  hrGlnProPheAla...GluValGlnLeuSer...AlaGluAspAlaCys 204
813  AACAACCATTTATGAGACCAGTACAAACTACTCAAGAGGAAGATGGCTGT 862

205  SerPheGlnPheProGluGluGluArgGlyGlyGluGlnThrGluGluLysCy 221
863  AGCTGCCGATTTCCAGAAGAAGAA..........GAAGGAGGATG 897

221  sHisLeu 223
898  TGAACTG 904
```

seq_name: N_Geneseq_34:Q75428

```
seq_documentation_block:
ID   Q75428 standard; cDNA to mRNA; 768 BP.
AC   Q75428;
DT   08-AUG-1995  (first entry)
DE   Murine 4-1BB polypeptide coding sequence.
KW   T-cell; lymphocyte; activation; tissue culture; clone; cell lines;
KW   proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine; ss.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   cds             1..768
FT                   /*tag=  a
FT                   /product= 4-1BB polypeptide.
FT   signal_peptide  1..69
FT                   /*tag=  b
```

FT   mat_peptide   70..768
FT   /*tag= c
PN   WO9426290-A.
PD   24-NOV-1994.
PF   06-MAY-1994; U05036.
PR   07-MAY-1993; US-060843.
PA   (IMMV) IMMUNEX CORP.
PI   Alderson MR, Goodwin RG, Smith CA;
DR   WPI; 95-022265/03.
DR   P-PSDB; R64199.
PT   Cytokine, 4-1BB ligand (4-1BB-L) - binds to cell surface receptor
PT   4-1BB to transduce signal
PS   Example 1; Page 43-44; 65pp; English.
CC   The 4-1BB polypeptide (receptor) and the 4-1BB-L (cytokine, see
CC   Q75422) are useful in a pharmaceutical composition for stimulating
CC   the immune system. The 4-1BB and 4-1BB-L polypeptides are also useful
CC   for exploring mechanisms of T-cell activation, as they are expressed
CC   on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for
CC   in vitro cultivation of primary T-cells during the derivation of
CC   clonal T-cell lines. It may also be used to stimulate proliferation
CC   of activated T-cells, used in therapeutic procedures.
CC   Sequence   768 BP;   188 A;   186 C;   217 G;   177 T;

alignment_scores:
     Quality: 153.50   Length: 219
     Ratio: 1.323   Gaps: 11
Percent Similarity: 52.968   Percent Identity: 27.854

alignment_block:
US-08-911-423-2 x Q75428

Align seg 1/1 to: Q75428 from: 1 to: 768

21 ProSerValValGluProGlyCysGlyProGlyLysValGlnAsnGl 37
    ::|||::|| ::|||:::|||
157 TCCAGCATAGGTGGACAGCCGAACTGT......................... 183

37 ySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaProGlyLysGluA 54
    ||| |||||||||::||||
184 ......AACATCTGCAGAGTGTGTGCAGGCTATTCAGGTTCAAGAAGT 226

54 spCysPro........LysGluArgCysIleCysValThrProGluTyr 67
    ||:|:   ::|:|| ||||| |||
227 TTTGCTCCCTCCTACCCACAACGCGGAGTGTGAGTGCATT...GAAGGATTC 273

68 HisCysGlyAspProGlnCysLysLysCysLysHisTyrProCysGlnPr 84
    ||||| ::||||||||||:: |||:::||
274 CATTGCTTGGGGCCACCAGTGCACCAGATGTGAAAAG...GACTGCAGGCC 320

84 oGlyGlnArgValGluSerGlnGlyAspIleGlyValPheGlyArgCysV 101
    |||||| ::: ||||||
321 TGGCCAGGAGCTAACGAAGCAGGGT.............TGCA 349

101 alAlaCysAlaMetGlyThrPheSerAlaGlyArgAsp...GlyHisCys 116
    :::||:||||:::||||||||:::
350 AAACCTGTAGCTTGGGAACATTTAATGACCAGAACGGTACTGGCGTCTGT 399

117 ArgLeuTrpThrAsnCysSerGlnPheGlyPheLeuThrMetPheProGl 133
    ||| ||||||||||||| ::|::| :::||
400 CGACCCTGGACGAACTGCTCTCTAGACGGAAGGTCTGTCTTAAGACCCGG 449

133 yAsnLysThrHisAsnAlaValCys.................... 141
    |:::::   ::::||||||
450 GACCACGGAGAAGGACGTGGTGTGGACCCCCTGTGGTGAGCTTCTCTC 499

142 ....IleProLeuProThrGluGlnTyr 151
    ::::::   :::
500 CCAGTACCACCATTCTGTGACTCCAGAGGGAGGACCAGGAGGCCACTCC 549

152 GlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePhe.. 167
    :::   :::||||||:::::::::::
550 TTGCAGGTCCTTACCTTGTTCCTTGGCCGTCGACTCGGCTTTGCTGCTGC 599

168 ....LeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgA 182
    :::|::::|||:::||| :::
600 CCTGATCTTCATTACTCTCCCTGTTCTCGTGCTCAAATGGATCAGGAAAA 649

182 rg...GlnHisMetCysProArgGluThrGlnProPheAlaGluValGln 197
    ::   ::||||||||| :::
650 AATTCCCCACATATTC........AAGCAACCATTTAAGAGAGACCACT 690

198 LeuSerAla.......GluAspAlaCysSerPheGlnPheProGluGluGl 212
    ::||| ||||||||||||| :::||||||
691 GGAGCAGCTCAAGAGGAGATGCTTGAGTGCCGATGCTGCCACAGGAAGA 740

212 uArgGly 214
    | |||
741 AGAAGGA 747

seq_name: N_Geneseq_34:T91027

seq_documentation_block:
ID   T91027 standard; cDNA to mRNA; 768 BP.
AC   T91027;
DT   25-FEB-1998 (first entry)
DE   Mouse 4-1BB receptor cDNA clone mu4-1BB.
KW   4-1BB ligand; 4-1BB-L; receptor; mouse; cytokine; T lymphocyte;
KW   T cell; proliferation; immunostimulant; ss.
OS   Mus musculus.
FH   Key   Location/Qualifiers
FT   sig_peptide   1..69
FT   /*tag= a
FT   mat_peptide   70..768
FT   /*tag= b
PN   US5674704-A.
PD   07-OCT-1997.
PF   07-MAY-1993; 060843.
PR   06-MAY-1994; US-236918.
PR   07-MAY-1993; US-060843.
PA   (IMMV) IMMUNEX CORP.
PI   Alderson MR, Goodwin RG, Smith CA;
DR   WPI; 97-502333/46.
DR   P-PSDB; W26659.
PT   DNA encoding 4-1BB ligand polypeptide(s) - useful for stimulating
PT   T-cell proliferation in vitro, and as research tools
PS   Disclosure; Column 39-40; 32pp; English.
CC   This cDNA clone encodes mouse 4-1BB (see W26659), a member of the
CC   tumour necrosis factor receptor superfamily that is expressed on
CC   helper, suppressor and cytolytic T lymphocytes, as well as mouse
CC   brain tissue. A novel claimed cytokine, designated 4-1BB ligand
CC   (4-1BB-L) has been identified, cloned and sequenced (see W26656)
CC   that binds to murine 4-1BB. 4-1BB-L, especially its soluble
CC   extracellular domain, can be used to stimulate T-cell proliferation
CC   in vitro, as a research tool and as an affinity ligand for
CC   purifying 4-1BB.
SQ   Sequence   768 BP;   188 A;   186 C;   217 G;   177 T;

alignment_scores:
     Quality: 153.50   Length: 219
     Ratio: 1.323   Gaps: 11
Percent Similarity: 52.968   Percent Identity: 27.854

alignment_block:
US-08-911-423-2 x T91027

Align seg 1/1 to: T91027 from: 1 to: 768

21 ProSerValValGluProGlyCysGlyProGlyLysValGlnAsnGl 37
    ::|||::|| ::|||:::|||
157 TCCAGCATAGGTGGACAGCCGAACTGT......................... 183

37 ySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaProGlyLysGluA 54
    ||| |||||||||::||||
184 ......AACATCTGCAGAGTGTGTGCAGGCTATTCAGGTTCAAGAAGT 226

PT Monoclonal antibody specific for human receptor protein 4-1BB - used
PT to enhance proliferation and activation of T-cells for treatment of
PT cancer and to inhibit specific ligand binding for treating
PT auto:immune diseases
PS Disclosure; Page 32-34; 48pp; English.
CC A cDNA clone (T39541) codes for novel murine receptor protein
CC 4-1BB (W04173), a protein that has the potential to function as
CC an accessory signaling molecule during T-cell activation and
CC proliferation. The cDNA clone was isolated and identified by
CC specific expression of T-cell genes. Primers (see also T39542-45)
CC based on the murine 4-1BB cDNA were utilised in the identification
CC of the gene (see also T39546) for the human homologue H4-1BB
CC (W04174), a protein used to raise a monoclonal antibody useful
CC in cancer and autoimmune disease therapy.
SQ Sequence 2347 BP;   590 A;   570 C;   580 G;   607 T;

alignment_scores:
        Quality: 153.50   Length: 219
        Ratio: 1.323   Gaps: 11
Percent Similarity: 52.968   Percent Identity: 27.854

alignment_block:
US-08-911-423-2 x T39541

Align seg 1/1 to: T39541 from: 1 to: 2347

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 21 ProSerValValGluGluProGlyCysGlyProGlyLysValGlnAsnGl 37
    :::||| :::|||
302 TCCAGCATAGGTGGACAGCCGAACTGT                        328

 37 ySerGlyAsnAsnThrArgCysCysSerLeuTyrAlaProGlyLysGluA 54
    ||| ||::: ||::||| :::|| :||
329 ...AACATCTGCAGAGTGTGCACAGTGTCCAGGCTATTCCAGGTTCAAGAAGT 371

 54 spCysPro........LysGluArgCysIleCysValThrProGluTyr 67
    ::::::| :::|||
372 TTTGCTCCTCTACCCACAACGCGGAGTGTGAGTGCATT...GAAGGATTC 418

 68 HisCysGlyAspProGlnCysLysLysHisTyrProCysGlnPr 84
    ::||| ||| :::||:||||
419 CATTGCTTGGGCCCACAGTGACCAGATGTGAAAAG...GACTGCAGGCC 465

 84 oGlyGlnArgValGluSerGlnGlyAspIleValPheGlyValPheArgCysV 101
    ||| |||
466 TGGCCAGGAGCTAACGAAGCAGGGT...TGCA                    494

101 alAlaCysAlaMetGlyThrPheSerAlaGlyArgAsp...GlyHisCys 116
    ||| ::: |||
495 AAACCTGTAGCTTGGGAACATTTAATGACCAGAACGTACTGGCGTCTGT 544

117 ArgLeuTrpThrAsnCysSerGlnPheLeuThrMetPheProGl 133
    ||| |||||||||| ||| ::|||
545 CGACCCTGGACGAACTGCTCTCTAGACGGAAGGTCTGTGCTTAAGACCCG 594

133 yAsnLysThrHisAsnAlaValCys.............. 141
    |:::| ||||
595 GACCACGGAGGAGGACGGTGGTGTTGGACCCCCTGTGTGAGCTTCTCTC 644

142 ............IleProGluProLeuProThrGluGlnTyr 151
    :||| |||
645 CCAGTACCACCATTTCTGACTCCAGAGGGAGGACCAGGAGGGCCACTCC 694

152 GlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePhe.. 167
    :||||||||||| ||| :::|||
695 TTGCAGGTCCTTACCTTGTTCCTGGCCGTGACATCGGCTTTGCTGCTGC 744

168 ......LeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgA 182
    :::||||| ::: ||| :::
745 CCTGATCTTCATTACTCCTGTTCTCTGTGCTCAAATGCAGGAAGAAA 794

182 rg...GlnHisMetCysProArgGluThrGlnProPheAlaGlyValGln 197
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 54 spCysPro........LysGluArgCysIleCysValThrProGluTyr 67
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227 TTTGCTCCTCTACCCACAACGCGGAGTGTGAGTGCATT...GAAGGATTC 273

 68 HisCysGlyAspProGlnCysLysLysHisTyrProCysGlnPr 84
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274 CATTGCTTGGGCCCACAGTGACCAGATGTGAAAAG...GACTGCAGGCC 320

 84 oGlyGlnArgValGluSerGlnGlyAspIleValPheGlyValPheArgCysV 101
    |||||| ::: |||
321 TGGCCAGGAGCTAACGAAGCAGGGT...............TGCA 349

101 alAlaCysAlaMetGlyThrPheSerAlaGlyArgAsp...GlyHisCys 116
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350 AAACCTGTAGCTTGGGAACATTTAATGACCAGAACGTACTGGCGTCTGT 399

117 ArgLeuTrpThrAsnCysSerGlnPheLeuThrMetPheProGl 133
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400 CGACCCTGGACGAACTGCTCTCTAGACGGAAGGTCTGTGCTTAAGACCGG 449

133 yAsnLysThrHisAsnAlaValCys.............. 141
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450 GACCACGGAGGAGGACGGTGGTGTGGACCCCCTGTGTGAGCTTCTCTC 499

142 ............IleProGluProLeuProThrGluGlnTyr 151
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500 CCAGTACCACCATTTCTGACTCCAGAGGGAGGACCAGGAGGGCCACTCC 549

152 GlyHisLeuThrValIlePheLeuValMetAlaAlaCysIlePhePhe.. 167
    ||||||||||||||||| :::|||||||
550 TTGCAGGTCCTTACCTTGTTCCTGGCCGTGACATCGGCTTTGCTGCTGG 599

168 ......LeuThrThrValGlnLeuGlyLeuHisIleTrpGlnLeuArgA 182
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600 CCTGATCTTCATTACTCCTGTTCTCTGTGCTCAAATGGATCAGGAAAA 649

182 rg...GlnHisMetCysProArgGluThrGlnProGluGluGlu 197
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650 AATTCCCCACCATATTC........AAGCAACCATTTAAGAAGACCACT 690

198 LeuSerAla......GluAspAlaCysSerSerPheGlnPheGlnGluG 212
    ::::||||| |||||
691 GGAGCAGCTCAAGAGAAGGAAGATGCTTGTAGCTGCCGATGTCCAAGGAAGA 740

212 uArgGly 214
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741 AGAAGGA 747
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seq_name: N_Geneseq_34:T39541

seq_documentation_block:
ID T39541 standard; cDNA to mRNA; 2347 BP.
AC T39541;
DT 12-DEC-1996 (first entry)
DE Mouse receptor 4-1BB cDNA.
KW Receptor 4-1BB; H4-1BB; monoclonal antibody; T-lymphocyte; T-cell;
KW immunostimulant; cancer; autoimmune disease; graft rejection;
KW therapy; ss.
OS Mus sp.
FH Key   Location/Qualifiers
FT cds   146..916
FT mat_peptide   146..913
FT   /*tag= a
FT   /*tag= b
PN WO9629348-A1.
PD 26-SEP-1996.
    U03965.
PF 22-MAR-1996; WO9629348.
PR 23-MAR-1995; US-409851.
PA (INDV) UNIV INDIANA FOUND.
PI Kang C, Kwon BS;
DR WPI; 96-443138/44.
DR P-PSDB; W04173.

Fri Aug 6 09:04:56 1999

795 AATTCCCCCACATATTC.........AAGCAACCATTTAAGAAGACCACT 835

198 LeuSerAla.......GluAspAlaCysSerPheGlnPheProGluGluGl 212
    :::::||| |||||||||||||| ::: |||:::|||||
836 GGAGCAGCTCAAGAGGAAGAGATGCTTGTAGCTGCCGATGTCCACAGGAAGA 885

212 uArgGly 214
    | |||
886 AGAAGGA 892